AMENDMENTS TO THE CLAIMS

1. - 43. (Canceled)

44. (Currently amended) A method of identifying a human having an increased risk for developing Alzheimer's disease, comprising determining the identity ~~detecting the presence~~ of a single nucleotide polymorphism (SNP) in said human's nucleic acids as represented by ~~at~~ position 101 of SEQ ID NO: 7368 or its complement ~~thereof in said human's nucleic acids~~, wherein ~~the presence of~~ C at position 101 of SEQ ID NO: 7368 or G at position 101 of the complement of SEQ ID NO: 7368 is indicative of an increased risk for Alzheimer's disease in said human.

45. (Previously presented) The method of claim 44 in which said human has Alzheimer's disease.

46. (Currently amended) The method of claim 44 in which SEQ ID NO: 7368 is contained within the genomic sequence of ~~as represented by~~ SEQ ID NO: 6756.

47. (Currently amended) The method of claim 44 in which the SNP ~~to be detected~~ is located at position 41788 of SEQ ID NO: 6756.

48. (Currently amended) The method of claim 44 in which said human's nucleic acids are extracted from a biological sample of said human ~~therefrom~~.

49. (Currently amended) The method of claim 48 in which said biological sample is blood, saliva, or buccal cells.

50. (Currently amended) The method of claim 44 in which said human's nucleic acids are amplified before the determining ~~detection~~ is carried out.

51. (Currently amended) The method of claim 44 in which the determining ~~detection~~ is carried out by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 55277, SEQ ID NO: 55278, and SEQ ID NO: 55279.

52. (Currently amended) The method of claim 44 in which the determining ~~detection~~ is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

53. (Currently amended) A method of identifying a human having a decreased risk for developing Alzheimer's disease, comprising determining the identity ~~detecting the presence~~ of a single nucleotide polymorphism (SNP) in said human's nucleic acids as represented by ~~at~~ position 101 of SEQ ID NO: 7368 or its complement ~~thereof in said human's nucleic acids~~, wherein ~~the presence of~~ T at position 101 of SEQ ID NO: 7368 or A at position 101 of the complement of SEQ ID NO: 7368 is indicative of a decreased risk for Alzheimer's disease in said human.

54. (Previously presented) The method of claim 44 in which said human has Alzheimer's disease.

55. (Currently amended) The method of claim 53 in which SEQ ID NO: 7368 is contained within the genomic sequence of ~~as represented by~~ SEQ ID NO: 6756.

56. (Currently amended) The method of claim 53 in which the SNP ~~to be detected~~ is located at position 41788 of SEQ ID NO: 6756.

57. (Currently amended) The method of claim 53 in which said human's nucleic acids are extracted from a biological sample of said human ~~therefrom~~.

58. (Currently amended) The method of claim 57 in which said biological sample is blood, saliva, or buccal cells.

59. (Currently amended) The method of claim 53 in which said human's nucleic acids are amplified before the determining ~~detection~~ is carried out.

60. (Currently amended) The method of claim 53 in which the determining ~~detection~~ is carried out by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 55277, SEQ ID NO: 55278, and SEQ ID NO: 55279.

61. (Currently amended) The method of claim 53 in which the determining ~~detection~~ is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

62. (Currently amended) A method of determining a human's risk for developing Alzheimer's disease, comprising determining the identity of ~~detecting~~ a single nucleotide polymorphism (SNP) in said human's nucleic acids as represented by ~~at~~ position 101 of SEQ ID NO: 7368 or its complement ~~thereof in said human's nucleic acids~~, wherein ~~the presence of~~ C at position 101 of SEQ ID NO: 7368 or G at position 101 of the complement of SEQ ID NO: 7368 is indicative of an increased risk for Alzheimer's disease in said human, or ~~the presence of~~ T at position 101 of SEQ ID NO: 7368 or A at position 101 of the complement of SEQ ID NO: 7368 is indicative of a decreased risk for Alzheimer's disease in said human.

63. (Previously presented) The method of claim 62 in which said human has Alzheimer's disease.

64. (Currently amended) The method of claim 62 in which SEQ ID NO: 7368 is contained within the genomic sequence of ~~LRP2 gene as represented by~~ SEQ ID NO: 6756.

65. (Currently amended) The method of claim 62 in which the SNP ~~to be detected~~ is located at position 41788 of SEQ ID NO: 6756.

66. (Currently amended) The method of claim 62 in which said human's nucleic acids are extracted from a biological sample of said human ~~therefrom~~.

67. (Currently amended) The method of claim 66 in which said biological sample is blood, saliva, or buccal cells.

68. (Currently amended) The method of claim 62 in which said human's nucleic acids are amplified before the determining ~~detection~~ is carried out.

69. (Currently amended) The method of claim 62 in which determining ~~detection~~ is carried out by using detection reagents comprising the nucleotide sequences of SEQ ID NO: 55277, SEQ ID NO: 55278, and SEQ ID NO: 55279.

70. (Currently amended) The method of claim 62 in which the determining ~~detection~~ is carried out by a process selected from the group consisting of: allele-specific probe hybridization, allele-specific primer extension, allele-specific amplification, sequencing, 5' nuclease digestion, molecular beacon assay, oligonucleotide ligation assay, size analysis, and single-stranded conformation polymorphism.

71. (New) The method of claim 62, further comprising providing a report of the identity of said SNP.

72. (New) The method of claim 62, further comprising providing a report of said human's increased risk for developing Alzheimer's disease.

73. (New) The method of claim 72, wherein the report further shows the identity of said SNP.

74. (New) The method of claim 73, wherein the identity of said SNP comprises C or its complement, and wherein the report indicates the increased risk for developing Alzheimer's disease.

75. (New) The method of claim 73, wherein the identity of said SNP comprises T or its complement, and wherein the report indicates the decreased risk for developing Alzheimer's disease.

76. (New) The method of any one of claims 71-75, wherein the report is in paper form or computer readable medium form.